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Sequence Listing could not be accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=12; day=2; hr=15; min=14; sec=30; ms=124;]

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Reviewer Comments:

<210> 9
<211> 527
<212> PRT
<213> protein p12 of T2 phage
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<210> 10
<211> 527
<212> PRT
<213> protein p12 of T4 phage
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<210> 11
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<212> PRT
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<212> PRT
<213> protein p12 of K3 phage
* * * * *

<210> 15
<211> 516
<212> PRT
<213> protein p12 of RB32-33 phage
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For SEQ ID # 9 through 15, numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." Please move any information that is not part of the "Genus/species" into a feature.

Application No: 10583415 Version No: 1.0

Input Set:**Output Set:**

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Finished: 2008-10-31 10:24:01.953
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 535 ms
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Total Errors: 0
No. of SeqIDs Defined: 15
Actual SeqID Count: 15

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SEQUENCE LISTING

<110> MEYER, ROMAN
 SCHUTZ, MICHAEL
 GRALLERT, HOLGER
 GRASSL, RENATE
 MILLER, STEFAN

<120> ENDOTOXIN DETECTION METHOD

<130> DEBE:067US

<140> 10583415
 <141> 2008-10-31

<150> PCT/DE2004/002778
 <151> 2004-12-20

<150> DE 103 60 844.3
 <151> 2003-12-20

<160> 15

<170> PatentIn version 3.3

<210> 1
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 <212> DNA
 <213> artificial sequence

<220>
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 aatacatatc aacacggtt 78

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<220>
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aatacatatc aacacggt 78

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<213> artificial sequence

<220>
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aatacatatc aacacggt 78

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<211> 19
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<213> artificial sequence

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<223> strep tag

<400> 5

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Thr Tyr Gln

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<211> 19
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<213> artificial sequence

<220>
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<400> 6

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Thr Tyr Gln

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<223> strep tag

<400> 7

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Thr Tyr Gln

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Thr	Tyr	Gln	His	Val	Ser	Asn	Glu	Ser	Arg	Tyr	Val	Lys	Phe	Asp	Pro
		20						25					30		

Thr	Asp	Thr	Asn	Phe	Pro	Pro	Glu	Ile	Thr	Asp	Val	Gln	Ala	Ala	Ile
	35						40					45			

Ala	Ala	Ile	Ser	Pro	Ala	Gly	Val	Asn	Gly	Val	Pro	Asp	Ala	Ser	Ser
50					55					60					

Thr	Thr	Lys	Gly	Ile	Leu	Phe	Leu	Ala	Thr	Glu	Gln	Glu	Val	Ile	Asp
65				70					75					80	

Gly	Thr	Asn	Asn	Thr	Lys	Ala	Val	Thr	Pro	Ala	Thr	Leu	Ala	Thr	Arg
		85						90					95		

Leu	Ser	Tyr	Pro	Asn	Ala	Thr	Glu	Ala	Val	Tyr	Gly	Leu	Thr	Arg	Tyr
		100					105					110			

Ser	Thr	Asp	Asp	Glu	Ala	Ile	Ala	Gly	Val	Asn	Asn	Glu	Ser	Ser	Ile	
		115					120					125				
Thr	Pro	Ala	Lys	Phe	Thr	Val	Ala	Leu	Asn	Asn	Val	Phe	Glu	Thr	Arg	
	130					135					140					
Val	Ser	Thr	Glu	Ser	Ser	Asn	Gly	Val	Ile	Lys	Ile	Ser	Ser	Leu	Pro	
145					150					155					160	
Gln	Ala	Leu	Ala	Gly	Ala	Asp	Asp	Thr	Thr	Ala	Met	Thr	Pro	Leu	Lys	
				165					170						175	
Thr	Gln	Gln	Leu	Ala	Val	Lys	Leu	Ile	Ala	Gln	Ile	Ala	Pro	Ser	Lys	
			180					185					190			
Asn	Ala	Ala	Thr	Glu	Ser	Glu	Gln	Gly	Val	Ile	Gln	Leu	Ala	Thr	Val	
		195					200					205				
Ala	Gln	Ala	Arg	Gln	Gly	Thr	Leu	Arg	Glu	Gly	Tyr	Ala	Ile	Ser	Pro	
	210					215					220					
Tyr	Thr	Phe	Met	Asn	Ser	Thr	Ala	Thr	Glu	Glu	Tyr	Lys	Gly	Val	Ile	
225					230					235					240	
Lys	Leu	Gly	Thr	Gln	Ser	Glu	Val	Asn	Ser	Asn	Asn	Ala	Ser	Val	Ala	
				245					250					255		
Val	Thr	Gly	Ala	Thr	Leu	Asn	Gly	Arg	Gly	Ser	Thr	Thr	Ser	Met	Arg	
			260					265						270		
Gly	Val	Val	Lys	Leu	Thr	Thr	Thr	Ala	Gly	Ser	Gln	Ser	Gly	Gly	Asp	
		275					280					285				
Ala	Ser	Ser	Ala	Leu	Ala	Trp	Asn	Ala	Asp	Val	Ile	His	Gln	Arg	Gly	
	290					295					300					
Gly	Gln	Thr	Ile	Asn	Gly	Thr	Leu	Arg	Ile	Asn	Asn	Thr	Leu	Thr	Ile	
305					310					315					320	
Ala	Ser	Gly	Gly	Ala	Asn	Ile	Thr	Gly	Thr	Val	Asn	Met	Thr	Gly	Gly	
				325					330						335	

Tyr	Ile	Gln	Gly	Lys	Arg	Val	Val	Thr	Gln	Asn	Glu	Ile	Asp	Arg	Thr	340	345	350
Ile	Pro	Val	Gly	Ala	Ile	Met	Met	Trp	Ala	Ala	Asp	Ser	Leu	Pro	Ser	355	360	365
Asp	Ala	Trp	Arg	Phe	Cys	His	Gly	Gly	Thr	Val	Ser	Ala	Ser	Asp	Cys	370	375	380
Pro	Leu	Tyr	Ala	Ser	Arg	Ile	Gly	Thr	Arg	Tyr	Gly	Gly	Ser	Ser	Ser	385	390	395
Asn	Pro	Gly	Leu	Pro	Asp	Met	Arg	Gly	Leu	Phe	Val	Arg	Gly	Ser	Gly	405	410	415
Arg	Gly	Ser	His	Leu	Thr	Asn	Pro	Asn	Val	Asn	Gly	Asn	Asp	Gln	Phe	420	425	430
Gly	Lys	Pro	Arg	Leu	Gly	Val	Gly	Cys	Thr	Gly	Gly	Tyr	Val	Gly	Glu	435	440	445
Val	Gln	Lys	Gln	Gln	Met	Ser	Tyr	His	Lys	His	Ala	Gly	Gly	Phe	Gly	450	455	460
Glu	Tyr	Asp	Asp	Ser	Gly	Ala	Phe	Gly	Asn	Thr	Arg	Arg	Ser	Asn	Phe	465	470	475
Val	Gly	Thr	Arg	Lys	Gly	Leu	Asp	Trp	Asp	Asn	Arg	Ser	Tyr	Phe	Thr	485	490	495
Asn	Asp	Gly	Tyr	Glu	Ile	Asp	Pro	Ala	Ser	Gln	Arg	Asn	Ser	Arg	Tyr	500	505	510
Thr	Leu	Asn	Arg	Pro	Glu	Leu	Ile	Gly	Asn	Glu	Thr	Arg	Pro	Trp	Asn	515	520	525
Ile	Ser	Leu	Asn	Tyr	Ile	Ile	Lys	Val	Lys	Glu						530	535	

<210> 9
 <211> 527
 <212> PRT
 <213> protein p12 of T2 phage

<400> 9

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val
20 25 30

Gln Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Leu Ala Thr Glu Gln
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Ala Val Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asp Asp Glu Ala Ile Ala Gly Val Asn Asn
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Val
115 120 125

Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Gln Leu Ala Val Lys Leu Ile Ala Gln Ile
165 170 175

Ala Pro Ser Lys Asn Ala Ala Thr Glu Ser Glu Gln Gly Val Ile Gln
180 185 190

Leu Ala Thr Val Ala Gln Ala Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr
210 215 220

Lys	Gly	Val	Ile	Lys	Leu	Gly	Thr	Gln	Ser	Glu	Val	Asn	Ser	Asn	Asn	
225					230					235					240	
Ala	Ser	Val	Ala	Val	Thr	Gly	Ala	Thr	Leu	Asn	Gly	Arg	Gly	Ser	Thr	
				245					250					255		
Thr	Ser	Met	Arg	Gly	Val	Val	Lys	Leu	Thr	Thr	Thr	Ala	Gly	Ser	Gln	
			260					265					270			
Ser	Gly	Gly	Asp	Ala	Ser	Ser	Ala	Leu	Ala	Trp	Asn	Ala	Asp	Val	Ile	
		275					280					285				
His	Gln	Arg	Gly	Gly	Gln	Thr	Ile	Asn	Gly	Thr	Leu	Arg	Ile	Asn	Asn	
	290					295					300					
Thr	Leu	Thr	Ile	Ala	Ser	Gly	Gly	Ala	Asn	Ile	Thr	Gly	Thr	Val	Asn	
305					310					315					320	
Met	Thr	Gly	Gly	Tyr	Ile	Gln	Gly	Lys	Arg	Val	Val	Thr	Gln	Asn	Glu	
				325					330					335		
Ile	Asp	Arg	Thr	Ile	Pro	Val	Gly	Ala	Ile	Met	Met	Trp	Ala	Ala	Asp	
			340					345					350			
Ser	Leu	Pro	Ser	Asp	Ala	Trp	Arg	Phe	Cys	His	Gly	Gly	Thr	Val	Ser	
		355					360					365				
Ala	Ser	Asp	Cys	Pro	Leu	Tyr	Ala	Ser	Arg	Ile	Gly	Thr	Arg	Tyr	Gly	
	370					375					380					
Gly	Thr	Ser	Ser	Asn	Pro	Gly	Leu	Pro	Asp	Met	Arg	Gly	Leu	Phe	Val	
385					390					395					400	
Arg	Gly	Ser	Gly	Arg	Gly	Ser	His	Leu	Thr	Asn	Pro	Asn	Val	Asn	Gly	
			405						410					415		
Asn	Asp	Gln	Phe	Gly	Lys	Pro	Arg	Leu	Gly	Val	Gly	Cys	Thr	Gly	Gly	
			420					425					430			
Tyr	Val	Gly	Glu	Val	Gln	Lys	Gln	Gln	Met	Ser	Tyr	His	Lys	His	Ala	
		435					440					445				

Gly Gly Phe Gly Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg
485 490 495

Asn Ser Arg Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
515 520 525

<210> 10
<211> 527
<212> PRT
<213> protein p12 of T4 phage

<400> 10

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val
20 25 30

His Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Ile Pro Thr Glu Gln
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Thr Val Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Asp Glu Ala Ile Ala Gly Val Asn Asn
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Ala
115 120 125

Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Gln Leu Ala Ile Lys Leu Ile Ala Gln Ile
165 170 175

Ala Pro Ser Glu Thr Thr Ala Thr Glu Ser Asp Gln Gly Val Val Gln
180 185 190

Leu Ala Thr Val Ala Gln Val Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Ser Ser Thr Glu Glu Tyr
210 215 220

Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn
225 230 235 240

Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr
245 250 255

Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln
260 265 270

Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile
275 280 285

Gln Gln Arg Gly Gly Gln Ile Ile Tyr Gly Thr Leu Arg Ile Glu Asp
290 295 300

Thr Phe Thr Ile Ala Asn Gly Gly Ala Asn Ile Thr Gly Thr Val Arg
305 310 315 320

Met Thr Gly Gly Tyr Ile Gln Gly Asn Arg Ile Val Thr Gln Asn Glu
325 330 335

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp
340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser
355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly
370 375 380

Gly Asn Pro Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val
385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly
405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly
420 425 430

Tyr Val Gly Glu Val Gln Ile Gln Gln Met Ser Tyr His Lys His Ala
435 440 445

Gly Gly Phe Gly Glu His Asp Asp Leu Gly Ala Phe Gly Asn Thr Arg
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Glu Ser Gln Arg
485 490 495

Asn Ser Lys Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
515 520 525

<210> 11
<211> 518
<212> PRT
<213> protein p12 of PP01 phage

<400> 11

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Lys Tyr Val
1 5 10 15

Lys Phe Asp Pro Val Gly Ser Asn Phe Pro Asp Thr Val Thr Thr Val

20

25

30

Gln Ser Ala Leu Ser Lys Ile Ser Asn Ile Gly Val Asn Gly Ile Pro
35 40 45

Asp Ala Ser Met Glu Val Lys Gly Ile Ala Met Ile Ala Ser Glu Gln
50 55 60

Glu Val Leu Asp Gly Thr Asn Asn Ser Lys Ile Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Leu Tyr Pro Asn Ala Thr Glu Thr Lys Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Glu Glu Thr Leu Glu Gly Ser Asp Asn
100 105 110

Asn Ser Ser Ile Thr Pro Gln Lys Leu Lys Tyr His Thr Asp Asp Val
115 120 125

Phe Gln Asn Arg Tyr Ser Ser Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Thr Pro Ala Ala Leu Ala Gly Val Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Lys Leu Ala Ile Lys Leu Ile Ser Gln Ile
165 170 175

Ala Pro Ser Glu Asp Thr Ala Ser Glu Ser Val Arg Gly Val Val Gln
180 185 190

Leu Ser Thr Val Ala Gln Thr Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195